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 GGGGGGAGGGGCGTGGGGGCAGGGAGCCGATTTGCATGCGGGCCGCCGCCGCCGCTG
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 TCTCCAAGCCCAGCTCTTTCCCCAAGGCTATGGAAACCACCAACAACCACTTCTACC
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 TTAGCACCCGCTTGACCACCATCACACGGGCACCCACCCGCTTCCCTGGGCACCGGGT
 TCCCATCCGGGCTAGCCCGCGCTCTACCACAGCACGGAACACTGCTGCCCTCCGACG
 GTCCTGTCCACCACGGCCCCCTTTCTTCAGTAGCAGCACGCCCGGCTCCCGACCCCGAT
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 GCACCAGCCCCAAATTTCACTACAACATACTCCACTGAACGATCTGAGCACTTCAA
 ACCCTGTGAGACAAGGACCTGGCGTATTGTCTCAATGATGGTGAATGCTTTGTGATT
 GAGACCCTGACAGGATCCCATAAGCACTGTCGGTGCAAGGAAGGCTACCAAGGAGTC
 CGTTGTGATCAATTTCTGCCGAAAACAGACTCCATCTTATCGGATCCAACAGACCACTT
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 GAAGAACAACAGGAAGTGAAAATATTACTAGAGACTGTGCAGGAACAGATCCGGATT
 CTGACTGATGCCAGACGGTCAGAAGACTTCGAACTGGCCAGCATGGAACTGAGGAC
 AGTGCAGCGGAAAACACAGCCTTTCTCCCCCTGAGTCCCACGGCCAAATCAGAACGAG
 AGGCACAATTTGTCTTAAGAAATGAAATACAAAGAGACTCTGTGCTAACCAAGTGACT
 GGAAATGTAGGAATCTGTGCATTATATGCTTTGCTAAACAGGAAGGAGAGGAAATTA
 AATACAAATTATTTATATGCATTAATTTAAGAGCATCTACTTAGAAGCC

Figure 1

TCACCGACCTAGTGGACTCCACTAGGTCGGTGGGCACGTA CTCTTGACGGAGCCCAC
CACGATCCATTTGAGAAGCATGAGGCGCGGCCCATGCCTCTGCCGCGGCCCTCGGGG
GGGCGAAGGTGAANACCGGCTCCTAGGATGAGTGAAGGGGCGGCCGCTGCCTCGCCA
CCTGGTGCCGCTTCGGCAGCCGCCGCTCGGCCGAGGAGGGCACCGCGCGGGCTGCG
GCGGCGGCAGCGGCGGGCGGGGCCCCGACGGCGGCGGCGAAGGGGCGGCCGAGCC
CCCCCGGAGTTACGCTGTAGCGACTGCATCGTGTGGAACCGGCAGCAGACGTGGCT
GTGCGTGGTACCTCTGTTTCATCGGCTTCATCGGCTGGGGCTCAGCCTCATGCTTCTCA
AATGGATCGTGGTGGGCTCCGTCAAGGAGTACGTGCCCCACCGACCTAGTGGACTCCAA
GGGGATGGGCCAGGACCCCTTCTTCTCTCCAAGCCCAGCTCTTTCCCCAAGGCCATG
GAGACCACCACCACTACCACTTCCACCACGTCCCCCGCCACCCCTCCGCCGGGGTG
CCGCCTCTCCAGGACGCCAACC GGATTAGCACTCGCCTGACCACCATCACGCGGGC
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GCACGGAACACTGCGGCCCTGCGACGGTCCCGTCCACCACGGCCCCGTTCTTCAGTA
GCAGCAGCTGGGCTCCCGACCCCGGTGCCAGGA ACTCCAAGTACCCAGGCAATGCC
CTCCTGGCCTACTGCGGCATACGCTACCTCCTCCTACCTTCACGATTCTACTCCCTCCT
GGACCTGTCTCCCTTTCAGGATGCTGCCTCCTCTTCTTCTCCTCCTCCTCCGCTA
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GATGGCGAGTGCTTTGTGATCGAAACCCTGACCGGATCCCATAAACACTGTGCGTGCA
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ACTCGAAGAATCAAGGATCCCAGACCAGGATACGATACCTTGCCAAGGGATAGAGGT
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TGCCTTCAAGAGAGACAAACCCCTATTTTAATAGCTTGGAGCAAAAGGACCTGGTGGG
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ACAACAAGAAGTGAAAATATTGCTAGAACTGTCCAGGAGCAGATCCGAATTCTGACT
GATGCCAGACGGTCAGAAGACTACGAACTGGCCAGCGTAGAAACCGAGGACAGTGCA
AGCGAAAACACAGCCTTTCTCCCCCTGAGTCCCACAGCCAAATCAGAACGAGAGGCGC
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GTAGGAATCTGTGCATTCTATGCTTTGCTCAACAGGAAAGAGAGGAAATCAAATACAA
ATTATTTATATGCATTAATTTAAGAGCATCTACTTAGAAGAAACCAAATAGTCTATCGC
CCTCATATCATAGTGTTTTTTAACAAAATATTTTTTTAAGGGAAAGAAATGTTTCAGGA
GGGATAAAGCTT

Figure 2

hNRG3B1 1 MSEGAAASPPGAASAAAASAEEGTAAAAAAAAAGGGPDGGGEGAAEPPR
mNRG3 1 MSEGAAASPPGAASAAAASAEEGTAAAAAAAAAGGGPDGGGEGAAEPPR

hNRG3B1 51 ELRCSDCIVWNRQQTWLCVVPLFIGFIGLGLSLMLLKWIVVGSVKEYVPT
mNRG3 51 ELRCSDCIVWNRQQTWLCVVPLFIGFIGLGLSLMLLKWIVVGSVKEYVPT

hNRG3B1 101 DLVDSKGMGQDPFFLSKPSSFPKAMETTTTTTTSTTSPATPSAGGAASSRT
mNRG3 101 DLVDSKGMGQDPFFLSKPSSFPKAMETTTTTTTSTTSPATPSAGGAASSRT

hNRG3B1 151 PNRISTRLTITRAPTRFPGHRVPIRASPRSTTARNTAAPATVPSTTAPF
mNRG3 151 PNRISTRLTITRAPTRFPGHRVPIRASPRSTTARNTAAPATVLPSTTAPF

hNRG3B1 201 FSSSTLGSRPPVPGTPTSTQAMPSPWPTAAYATSSYLHDSTPSWTLSPFQD-
mNRG3 201 FSSSTPGSRPPMPGAPSTQAMPSPWPTAAYATSSYLHDSTPSWTLSPFQDA

hNRG3B1 250 -AASSSSSSSSSATTTTTPETSTSPKFHTTYS TERSEHFKEPRDKDLAYD
mNRG3 251 A-AASSSSPSSTSTTTTTPETSTSPKFHTTYS TERSEHFKEPRDKDLAYD

hNRG3B1 299 LNDGEQFVIETLTGSHKHQRCKEGYQGVREDDQFLPKTDSILSDPTDHLGI
mNRG3 301 LNDGEQFVIETLTGSHKHQRCKEGYQGVREDDQFLPKTDSILSDPTDHLGI

hNRG3B1 349 EFMESEEVYQROVLSISCIIFGIVIVGMFCAAFYFKSKKOAKOIQEQLKV
mNRG3 351 EFMESEEVYQROVLSISCIIFGIVIVGMFCAAFYFKSKKOAKOIQEHLKE

hNRG3B1 399 PQNGKSYSLKASSTMAKSENLVKSHVQLQNYSKVERHPVTALEKMMESSF
mNRG3 401 SQNGKNYSLKASST--KSESLMKSHVHLQNYSKADRHHPVTALEKIMESSF

hNRG3B1 449 VGPQSFPEVPSPDRGSQSVKHHRSLSGCCSPGQSGMLHRNAFRRTPPSP
mNRG3 449 SAPQSFPEVTSPDRGSOPIKHH-----SPGQSGMLHRNTERRAPPSP

hNRG3B1 499 RSRLGGIVGPAYQOLEESRIPDQDITPCQGIEVRKTISHLP IQLWCVERP
mNRG3 492 RSRLGGIVGPAYQOLEESRIPDQDITPCQGIEVRKTISHLP IQLWCVERP

hNRG3B1 549 LDKYSISGLKTRNTSINMQLPSRETNPYFNSEQKDLVGYSSTRASSV
mNRG3 542 LDKYVSNGLRTOQNASINMQLPSRETNPYFNSEQKDLVGYSSTRANSV

hNRG3B1 599 PIIPSVGLEETCLQMPGISLVKSIKWCKNSYSADVNVVSIIPVSDCLIAEQ
mNRG3 592 PIIPSMGLEETCMQMPGISLVKSIKWCKNSYSADIVNISMVSDCVIEEQ

hNRG3B1 649 QEVKILLETVQEQIRILTDARRSEDYELASVETEDSASENTAFLPLSPTA
mNRG3 642 QEVKILLETVQEQIRILTDARRSEDFELASMETEDSASENTAFLPLSPTA

hNRG3B1 699 KSEREAQFVLRNEIQRDSALTK
mNRG3 692 KSEREAQFVLRNEIQRDSVLTk

Figure 4A

hNRG3.egf	288	HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRC-DQFL
cARIA.egf	137	HLTKCDIKQKAFQVNGGECYMKDLPNPPRYLCRCPNEFTGDRC-QNYV
hAR.egf	142	KKNPCNAEFQNECIE-GECKYIEHLEAVT---CKCQQETFGERCGEKSM
hBTC.egf	65	HFSRCPKQYKHYCIK-GRCRFVVAEQTPS---CVCDEGYIGARCERVDL
hEGF.egf	972	SDSECPLSHDGYCLHDGVCMYIEALDKYA---CNCVVGYYIGERCQYRDL
hHB-EGF.egf	104	KRDPCLRKYKDFCIH-GECKYVKELRAPPS---CICHPGYHGERCHGLSL
hHRGα.egf	178	HLVKCAEKEKTFQVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTENYP
hHRGβ.egf	178	HLVKCAEKEKTFQVNGGECFMVKDLSNPSRYLCKCQNEFTGDRC-QNYV
hTGFα.egf	43	HFNDCPDSHTQECFH-GTCRFLVQEDKPA---CVCHSGYVGARCEHADL
mEPR.egf	57	QITKCSSDMDGYCLH-GQCIIYLVDMREKF---CRCEVGYTGLRCEHFFL

Figure 5

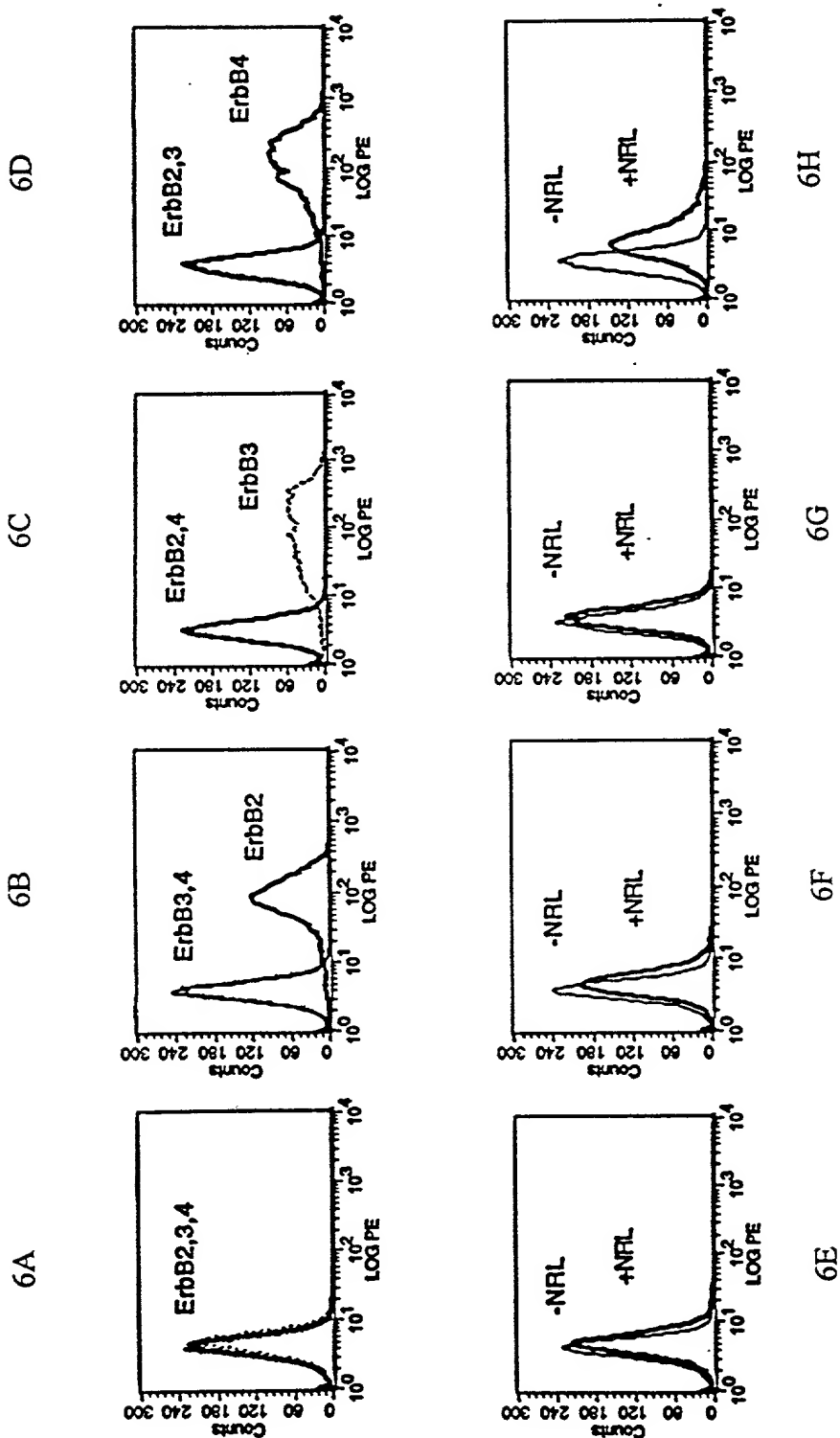


Figure 6A - 6H

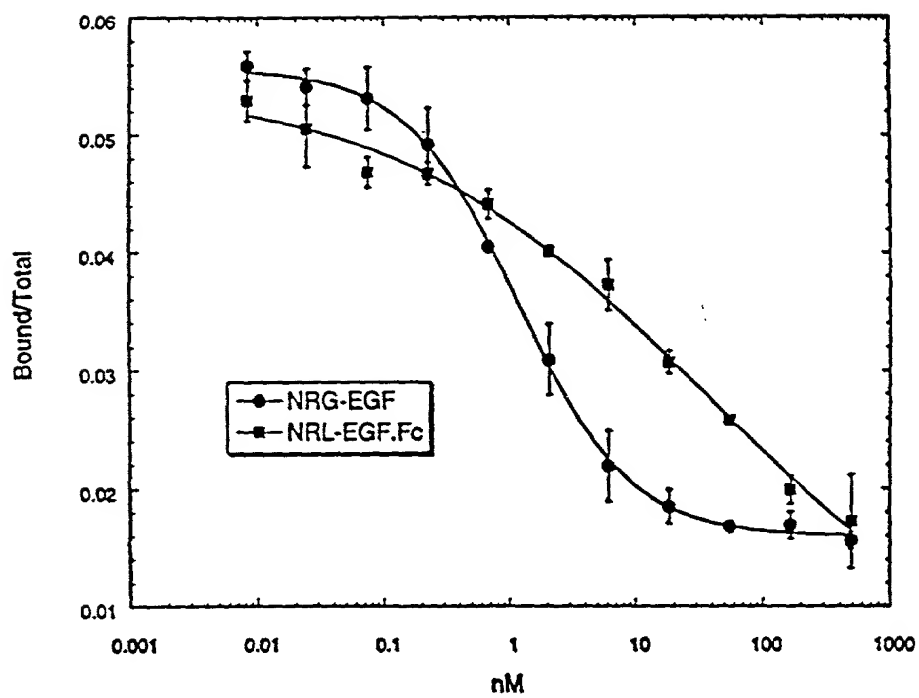


Figure 7